Figure 3 represents the S. cerevisiae ELO2 sequence (SEQ ID NO:9) homologous to the jojoba KCS sequence (primer sequence underlined) of Figure 2.

Figure 4A shows the physical map of pRAE-2 containing the MAELO cDNA. Figure 4B represents the physical map of the constitutive expression vector, pRAE-5, used for elongase enzyme production in yeast.

Figure 5 represents a comparison of the nucleotide sequences of clones pRAE-5 (SEQ ID NO:10) and pRAE-6 (SEQ ID NO:11).

Figure 6 illustrates the complete nucleotide sequence of Mortierella alpina elongase (MAELO) (SEQ ID NO:1).

Figure 7 represents the amino acid sequence of the Mortierella alpina elongase (SEQ ID NO:12) translated from MAELO (see Figure 6).

Figure 8 represents an amino acid sequence alignment among 3 elongases: S. cerevisiae ELO2 (GNS1)(SEQ ID NO:13), S. cerevisiae ELO3 (SUR4) (SEQ ID NO:14) and the translated MAELO sequence as shown in Figure 7.

Figure 9 represents a comparison between the nucleotide sequence MAELO (SEQ ID NO:15) and the nucleotide sequence of ELO2 from S. cerevisiae (SEQ ID NO:16).

Figures 10A and 10B represents the PUFA elongase activity of MAELO expressed in baker's yeast.

Figure 11 illustrates the PUFA elongase activity of MAELO when co-expressed with the Δ5-desaturase cDNA from M. alpina to produce AA.

Figure 12 compares the PUFA elongase activity of MAELO to the overexpression of ELO2 from S. cerevisiae in baker's yeast.

Figures 13 (SEQ ID NO:17 and SEQ ID NO:18), 14 (SEQ ID NO:19 and SEQ ID NO:20) and 15 (SEQ ID NO:21 and SEQ ID NO:22) represent three separate comparisons of amino acid sequences (SEQ ID NO:17, SEQ ID NO:19 and SEQ ID NO:21) derived from C. elegans

nucleotide sequences in the GenEMBL database with the translated MAELO (SEQ ID NO:18, SEQ ID NO:20 and SEQ ID NO:22).

Figure 16 shows the comparison between amino acid translations of two different mammalian sequences in the GenEMBL database (SEQ ID NO:23 and SEQ ID NO:26) and the translated MAELO (SEQ ID NO:24 and SEQ ID NO:25).

Figure 17 shows the comparison of a translated DNA sequence (see published PCT application WO 88/07577)(SEQ ID NO:28) with the amino acid sequence derived from MAELO (SEQ ID NO:27), which was detected during a database search.

Figure 18 shows the complete amino acid sequence of the Δ5-desaturase from M. alpina (SEQ ID NO:29).

Figure 19 represents the initial GC-FAME analysis of MAD708 pool. The detection of a DGLA (C20:3n-6) peak should be noted.

Figure 20 represents the PUFA elongase activity of the five MAD708 clones in yeast with GLA as substrate. All clones have apparent elongase activity.

Figure 21 represents the DNA sequencing analysis of plasmid pRPB2. The analysis reveals an open reading frame of 957 bp in length.

Figure 22 shows the complete nucleotide sequence of the M. alpina cDNA (SEQ ID NO:2), contained in the plasmid pRPB2, which is designated GLELO for its GLA elongase activity.

Figure 23 represents the amino acid sequence of the M. alpina elongase (SEQ ID NO:30) translated from GLELO (see Figure 22).

Figure 24 illustrates the n-6 PUFA elongase activity in an induced culture of 334(pRPB2) when supplemented with GLA.

Figure 25 represents the n-3 and n-6 PUFA elongase activity in an induced culture of 334(pRPB2) when supplemented with 25 μm of other fatty acid substrates.

Figure 26A illustrates the elongase activity of GLELO with GLA as a substrate when co-expressed with the M. alpina Δ5-

desaturase cDNA to produce AA. Figure 26B illustrates the elongase activity of GLELO with STA as a substrate when co-expressed with the M. alpina Δ5-desaturase cDNA to produce EPA.

Figure 27 illustrates the comparison between the translated GLELO sequence (SEQ ID NO:31) (see Figure 23) and the translated MAELO sequence (SEQ ID NO:32) (see Figure 7).

Figure 28 represents a comparison of the amino acid sequence of 4 elongases: the translated amino acid sequence of GLELO (see Figure 23), MAELO (see Figure 7), S. cerevisiae ELO2 (GNS1), and S. cerevisiae ELO3 (SUR4). The histidine box is underlined.

Figure 29 represents an alignment between translated MAELO sequence (SEQ ID NO:33) and translated putative human homologue HS1 sequence (SEQ ID NO:34).

Figure 30 represents an alignment between the translated MAELO sequence (SEQ ID NO:35) and the translated putative human homologue HS2 sequence (SEQ ID NO:36).

Figure 31 shows an alignment between the translated MAELO sequence (SEQ ID NO:35) and the translated putative mouse homologue MM2 sequence (SEQ ID NO:36).

Figure 32 represents an alignment between the translated MAELO sequence (SEQ ID NO:39) and the translated putative mouse homologue AI225632 sequence (SEQ ID NO:40).

Figure 33 illustrates an alignment between the translated GLELO sequence (SEQ ID NO:41) and the translated human homologue AI815960 sequence (SEQ ID NO:42).

Figure 34 shows an alignment between the translated GLELO sequence (SEQ ID NO:43) and the translated putative human homologue HS1 sequence (SEQ ID NO:44).

Figure 35 represents an alignment between the translated GLELO sequence (SEQ ID NO:45) and the translated putative human homologue sequence from AC004050 (SEQ ID NO:46).

Figure 36 illustrates an alignment between the translated GLELO sequence (SEQ ID NO:47) and the translated putative mouse homologue MM2 sequence (SEQ ID NO:48).

Figure 37 represents an alignment of the translated GLELO sequence (SEQ ID NO:49) and a translated putative mouse homologue AI225632 sequence (SEQ ID NO:50).

Figure 38 illustrates an alignment of the translated GLELO sequence (SEQ ID NO:51) and a translated putative mouse homologue U97107 (SEQ ID NO:52).

Figure 39 represents an alignment of the translated GLELO sequence (SEQ ID NO:53) and a translated putative C. elegans U68749 (F56H11.4) homologue sequence (SEQ ID NO:54).

Figure 40 shows an alignment between the translated MAELO sequence and a translated putative C. elegans U68749 (F56H11.4) homologue sequence (SEQ ID NO:55).

Figure 41 represents an alignment between the translated GLELO sequence (SEQ ID NO:55) and a translated putative Drosophila melanogaster homologue sequence, DM1 (SEQ ID NO:57).

Figure 42 illustrates an alignment between the translated MAELO (SEQ ID NO:58) sequence and a translated putative Drosophila melanogaster homologue sequence, DM1 (SEQ ID NO:59).

Figure 43 illustrates the complete nucleotide sequence of a human elongase HSELO1 (SEQ ID NO:3).

Figure 44 represents the deduced amino acid sequence of the human elongase HSELO1 (SEQ ID NO:60).

Figure 45 illustrates the elongase activity (PUFA and others) of an induced culture of 334(pRAE-58-A1) when supplemented with GLA or AA.

Figure 46 shows the complete nucleotide sequence of the C. elegans elongase CEELO (SEQ ID NO:4).

Figure 47 represents the deduced amino acid of C. elegans elongase CEELO (SEQ ID NO:55).

Figure 48 illustrates the PUFA elongase activity of an induced culture of 334(Trêt-21) and 334(Trêt-22) when supplemented with GLA and AA.

Figure 49 represents the complete nucleotide sequence of the putative human elongase gene HS3 (SEQ ID NO:61).

Figure 50 illustrates the deduced amino acid sequence of the putative human elongase enzyme HS3 (SEQ ID NO:62).

Figure 51 represents the elongase activity (PUFA and others) of HSELO1 expressed in baker's yeast when supplemented with GLA, AA, STA, EPA, OA, or ALA.

Figure 52 represents the elongase activity (PUFA and others) of HSELO1 expressed in baker's yeast when supplemented with 25 mM or 100 mM of GLA, AA, or EPA.

Figures 53A, 53B, and 53C represent the elongase activity (PUFA and others) of HSELO1 expressed in baker's yeast when supplemented with PA, SA, ARA, BA, PTA, OA, EA, LA, GLA, DGLA, AA, ADA, ALA, STA, EPA, or DPA, or when no substrate is present.

Figure 54 represents the complete nucleotide sequence of mouse elongase MELO4 (SEQ ID NO:5).

Figure 55 represents the deduced amino acid sequence of the mouse elongase MELO4 (SEQ ID NO:63).

Figure 56 represents the PUFA elongase activity of MELO4 expressed in baker's yeast when supplemented with GLA, AA, ADA, STA, EPA, or DPA.

Figures 57A, 57B, and 57C represent the PUFA elongase activity of MELO4 expressed in baker's yeast when supplemented with PA, SA, ARA, BA, PTA, OA, EA, LA, GLA, DGLA, AA, ADA, ALA, STA, EPA, or DPA, or when no substrate is present.

Figure 58 represents the complete nucleotide sequence of mouse elongase MELO7 (SEQ ID NO:6).

Figure 59 represents the deduced amino acid sequence of the mouse elongase MELO7 (SEQ ID NO:64).

Figure 60 represents the elongase activity (PUFA and others) of MELO7 expressed in baker's yeast when supplemented with GLA, AA, ADA, STA, EPA, or DPA.

Figure 61 shows the activity of the C. elegans elongase when expressed in yeast when no substrate is present and with addition of AA or GLA.

Figure 62 illustrates the PUFA elongase activity of an induced culture of 334(pRET22) when supplemented with 50 mM of various substrates.

Figure 63 represents the PUFA elongase activity with GLA (Figure 63A) or STA (Figure 63B) as a substrate when co-expressed with the M. alpina Δ5-desaturase cDNA to produce AA or EPA, respectively.

Please replace the paragraph on page 58, line 6 - page 58, line 29 with the following paragraph:

The β-ketoacyl-coenzyme A synthase (KCS) from jojoba and the Saccharomyces cerevisiae elongase (ELO2) were aligned to determine an area of amino acid homology (see Figure 2). The codon bias was applied to the area of sequence corresponding to the homologous amino acids between the two elongases, and primers were designed based on this biased sequence (see Figure 3). The cDNA was excised from the M11 M. alpina cDNA library (Knutzon et al., J. Biol. Chem. 273:29360-29366 (1998)), which contains approximately 6 X 10^5 clones with an average insert size of 1.1 Kb. The excised cDNA was amplified with internal primer RO339 (5' -**TTG GAG AGG AGG AAG CGA CCA CCG AAG ATG ATG**- 3') (SEQ ID NO:65) and a vector forward primer RO317 (5'- **CAC ACA GGA AAC AGC TAT GAC CAT GAT TAC G** -3') (SEQ ID NO:66). Polymerase Chain Reaction (PCR) was carried out in a 100 ③l volume containing: 300 ng of excised M. alpina cDNA library, 50 pmole each primer, 10 µl of 10X buffer, 1 µl 10 mM PCR Nucleotide Mix (Boehringer Mannheim Corp., Indianapolis, IN) and 1.0 U of Taq Polymerase. Thermocycler conditions in Perkin Elmer 9600 (Norwalk, CT) were as follows: 94°C

for 2 mins., then 30 cycles of 94°C for 1 min., 58°C for 2 mins., and 72°C for 3 mins. PCR was followed by an additional extension at 72°C for 7 minutes.

Please replace the paragraph bridging page 59-60 (i.e., page 59, line 12 - page 60, line 26) with the following paragraph:

New primers were designed based on the putative elongase sequence and the vector, pZL1 (Life Technologies, Inc., Gaithersburg, MD) sequence used to construct M. alpina cDNA library. The M. alpina excised cDNA library was PCR amplified again using primers RO350 (5' -**CAT CTC ATG GAT CCG CCA TGG CCG CCG CAA TCT TG-** 3') (SEQ ID NO:67), which has an added *BamHI* restriction site (underlined), and the vector reverse primer RO352 (5' - ACG CGT ACG TAA AGC TTG- 3') (SEQ ID NO:68) to isolate the full length M. alpina elongase cDNA, using previously described conditions. The termini of the approximately 1.5 Kb PCR amplified fragment was filled-in with T4 DNA polymerase (Boehringer Mannheim Corp., Indianapolis, IN) to create blunt ends and cloned into the pCR-blunt vector (Invitrogen Corp., Carlsbad, CA). This resulted in two clones, pRAE-1 and pRAE-2 (see Figure 4A). (Plasmid DNA pRAE-2 was deposited with the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209, on August 28, 1998, under the terms of the Budapest Treaty, and was accorded deposit number ATCC 203166.) The elongase cDNAs from these vectors were cut out as an *EcoRI* fragment and cloned into the *EcoRI* digested pYX242 (Novagen, Madison, WI) vector. The clones pRAE-5 and pRAE-6 (see Figure 4B) have the elongase cDNAs from pRAE-1 and pRAE-2, respectively. (Plasmid DNA pRAE-5 was deposited with the American Type

Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209, on August 28, 1998, under the terms of the Budapest Treaty, and was accorded deposit number ATCC 203167.) The sequencing of pRAE-5 and pRAE-6 revealed that 5' untranslated region of the elongase gene in pRAE-5 is 16 bp shorter than that in pRAE-6 (see Figure 5). The complete M. alpina elongase cDNA sequence, designated MAELO was obtained from pRAE-2 (see Figure 6). Figure 7 is the amino acid sequence obtained from the translation of MAELO. The Swissprot database (GeneBio, Geneva, Switzerland) was searched again, as previously described, with the translated MAELO: MAELO has 44.3% identity in 317 amino acids with S. cerevisiae GNS1(ELO2) and 44.7% identity in 318 amino acids with S. cerevisiae SUR4(ELO3). The FastA alignment among the three elongases is shown in Figure 8. At the nucleotide level (see Figure 9), MAELO has 57.4% identity in 549 bp overlap with S. cerevisiae GNS1(ELO2) (GenBank Accession # S79624). However, the identity between the complete MAELO gene of 954 bp and S. cerevisiae GNS1(ELO2) is 33.0%.

Please replace the paragraph bridging pages 63-64 (i.e., page 63, line 7 - page 64, line 4) with the following paragraph:

The ELO2 gene encoding for the yeast elongase was cloned from an S. cerevisiae genomic library (Origene, Rockville, MD) using the primers RO514 (5' -**GGC TAT GGA TCC ATG AAT TCA CTC GTT ACT CAA TAT G**-3') (SEQ ID NO:69) and RO515 (5' -**CCT GCC AAG CTT TTA CCT TTT TCT TCT GTG TTG AG**-3') (SEQ ID NO:70) incorporating the restriction sites (underlined) *BamHI* and *Hind*III

(respectively). The ELO2 gene was cloned into the vector pYX242 at the *BamHI* and *Hind*III sites, designated pRELO, transformed into the S. cerevisiae host 334 (Hoveland et al., supra) and screened for PUFA elongase activity. The vector plasmid was used as a negative control and 334(pRAE-5) was grown to compare the PUFA elongase activity. The cultures were grown as previously described with no galactose in the media and 25 μM GLA added as a substrate. Figure 12 shows that amount of 20:3n-6 or DGLA produced (elongated from 18:3n-6 or GLA) by 334(pRAE-5) was approximately 4 times the negative control containing the unaltered vector pYX242, while the two individual clones 334(pRELO-1) and 334(pRELO-2) were only twice the negative control. Additionally, when DGLA produced is expressed as a percent of the total lipids (shown in parenthesis, Figure 12), the clones 334(pRELO-1) and 334 (pRELO-2) produced 0.153% and 0.2% DGLA respectively, while 334(pYX242) produced 0.185% DGLA. Hence all these strains produced comparable percentages of DGLA. The strain 334(pRAE-5), however, produced 0.279% DGLA, an increase of 50.8% over 334(pYX242) (negative control). These data show that the S. cerevisiae elongase gene ELO2, even when overexpressed in yeast, does not elongate GLA to DGLA effectively. The M. alpina PUFA elongase activity is specific for this conversion as evidenced by the higher amount of DGLA produced compared to the control, 334(pYX242).

Please replace the paragraph bridging pages 74 - 75 (i.e., page 74, line 13 - page 75, line 21) with the following paragraph:

The plasmid DNAs isolated from yeast were re-amplified in E. coli for long-term storage of the cDNA clones as well as for DNA sequencing. E. coli TOP10 (Invitrogen Corp., Carlsbad, CA) cells

were transformed with the pRPB recombinant plasmids according to the manufacturer's protocol. The transformants obtained from each plasmid DNA were inoculated into LB containing ampicillin (50 µg/ml) and grown overnight at 37 °C with shaking. Plasmid DNAs were isolated from these cultures by using QIAprep Spin Miniprep (Qiagen Inc., Valencia, CA) according to the manufacturer's protocol. The purified plasmid DNAs were then used for sequencing from both 5' and 3' ends. The DNA sequencing was performed by using a 373A Stretch ABI automated DNA sequencer (Perkin Elmer, Foster City, CA) according to the manufacturer's protocol. Primers used for sequencing were the forward primer RO541 (5'- **GAC TAC TAG CAG CTG TAA TAC** -3') (SEQ ID NO:71) and the reverse primer RO540 (5'- **GTG AAT GTA AGC GTG ACA TAA** -3') (SEQ ID NO:72) contained in the multicloning sites of the pYES2 vector. The obtained nucleotide sequences were transferred to Sequencher software program (Gene Codes Corporation, Ann Arbor, MI) for analysis. The DNA sequence analysis revealed that all five elongase cDNAs contained the identical nucleotide sequence with a common overlap of 301 nucleotides. Each DNA sequence contains a putative start site at the beginning of the 5' end and a stop codon with poly A tail at the end of the 3' site. To further confirm the DNA sequence, internal forward primers RO728 (5'- **GAG ACT TTG AGC GGT TCG** -3') (SEQ ID NO:73) and RO730 (5'- **TCT CTG CTG CGT TGA ACT CG** -3') (SEQ ID NO:74), along with reverse primers RO729 (5'- **AAA GCT CTT GAC CTC GAA C** -3') (SEQ ID NO:75) and RO731 (5'- **AAC TTG ATG AAC GAC ACG TG** -3') (SEQ ID NO:76) were designed within the cDNA, and used for sequencing of pRPB2, since this candidate possessed the highest elongase activity. The entire nucleotide sequence was analyzed by the Sequencher program (Figure 21), and the longest open reading frame deduced from the entire cDNA sequence in pRPB2 appeared to be 957 bp in length (Figure 22). The deduced open reading frame

was then translated into the corresponding amino acid sequence, and the predicted sequence is shown in Figure 23. The elongase encoded by the cDNA (pRPB2) identified from M. alpina appears to be a 318 amino acid long protein which is nearly identical in size with translated MAELO. This new elongase cDNA was designated as "GLELO" and its encoded protein has been named "GLA elongase".

Please replace the paragraph bridging pages 79 - 80 (i.e., page 79, line 28 - page 80, line 24 with the following paragraph:

The National Center for Biotechnology Information (NCBI at ~~http://www.~~ncbi.nlm.nih.gov/) was used to conduct database searches using tblastn with the 28 amino acid sequence (**DTIFIILRKQKLIFLHWYHHITVLLYSW**) (SEQ ID NO:87) translated from AC004050 (a human sequence identified in a TfastA search, see Example V). This amino acid sequence contains a histidine box (underlined), which has a noted motif of desaturases (Knutzon et al., supra), and both PUFA elongases, MAELO and GLELO (see Figure 23). A translated mouse sequence shown previously in Example V (GenBank Accession #U97107) and a translated C. elegans sequence (GenBank Accession # U41011) had the highest matches with this 28 amino acid query. The NCBI mouse EST database was searched again with tblastn, using translated U41011 as a query. An additional mouse sequence was identified (GenBank Accession #AF014033.1), annotated as "putative involvement in fatty acid elongation." Three longer sequences (GenBank Accession #'s AA591034, AA189549, and AA839346) were identified through a tblastn search of the mouse EST database with translated AF014033.1 and combined into one sequence designated as mm2. The FastA alignment (see Example I) of translated mm2 and MAELO is shown in Figure 31. Another related, but not identical mouse sequence (GenBank Accession

#AI225632), was also identified in a tblastn search of the mouse EST database with AF014033.1. The FastA alignment with translated AI225632 to MAELO is shown in Figure 32. The percent identity for both translated MM2 and AI 225632 with translated MAELO is 30.4% in 191 and 115 amino acid overlap, respectively. The level of amino acid identity with translated MAELO with these two translated mouse sequences identifies them as putative homologues of PUFA elongases.

Please replace the paragraph bridging page 84 - page 85 (i.e., page 84, line 31 - page 85, line 12) with the following paragraph:

Primers RO719 (5' -**GGT TCT CCC ATG GAA CAT TTT GAT GCA TC-** 3') (SEQ ID NO:77) and RO720 (5' -**GGT TTC AAA GCT TTG ACT TCA ATC CTT CCG-** 3') (SEQ ID NO:78) were designed based on the putative HS1 sequence, and used to amplify the human liver Marathon-Ready cDNA (Clontech Laboratories, Inc., Palo Alto, California). The polymerase Chain Reaction (PCR) was carried out in a 50 µl volume containing: 5 µl of human liver Marathon-Ready cDNA, 50 pmole each primer, 1 µl 10 mM PCR Nucleotide Mix (Boehringer Mannheim Corp., Indianapolis, IN), 5 µl 10 X buffer and 1.0 U of Advantage KlenTaq Polymerase Mix (Clontech Laboratories, Inc., Palo Alto, CA). Thermocycler conditions in Perkin Elmer 9600 (Norwalk, CT) were as follows: 94 °C for 2 mins, then 30 cycles of 94 °C for 1 min., 58 °C for 2 mins, and 72 °C for 3 mins. PCR was followed by an additional extension cycle at 72 °C for 7 minutes.

Please replace the paragraph bridging pages 89 - 90 (i.e., page 89, line 15 - page 90, line 2) with the following paragraph:

Several putative C. elegans elongases were identified with amino acid homology to both translated GLELO and MAELO. As with the human cDNA sequence, cloning of a cDNA and expression in yeast was used to determine if indeed it was a PUFA elongase. Primers RO738 (5′ -**AAT CAG GAA TTC ATG GCT CAG CAT CCG CTC GTT CAA C** -3′) (SEQ ID NO:79) and RO739 (5′ -**CCG CTT GTC GAC TTA GTT GTT CTT CTT CTT TGG CAC** -3′) (SEQ ID NO:80) with restriction sites *EcoRI* and *SalI* (underlined), respectively, were based on the putative cDNA sequence contained in the genomic sequence U68749 (wormpep cDNA accession #F56H11.4.) A PCR amplification was performed in a 100 µl volume containing: 250 ng excised C. elegans library cDNA (OriGene Technologies Inc., Rockville, MD), 50 pmole each primer, 10 µl 10X reaction buffer (Boehringer Mannheim Corp., Indianapolis, IN), 1 µl 10 mM PCR Nucleotide mix (Boehringer Mannheim Corp., Indianapolis, IN), and 2.5 U Taq polymerase (Boehringer Mannheim Corp., Indianapolis, IN). Thermocycler conditions in a Perkin Elmer 9600 (Norwalk, CT) were as follows: 95 °C for 5 mins, then 25 cycles of 94 °C for 30 secs, 55 °C for 2 mins, and 72 °C for 2 mins. PCR was followed by an additional cycle of 72 °C for 7 minutes.

Please replace the paragraph on page 92, lines 17-29 with the following paragraph:

To isolate the full length putative elongase cDNA based on the AC004050 sequence, primers RP735 (5′ -**CCT CCT GAA TTC CAA CAC TAT TCA GCT TTC** -3′) (SEQ ID NO:81) and RO73 (5′ -**TAA TAC GAC TCA CTA TAG GG** -3′) (SEQ ID NO:82) were used to PCR amplify the human liver Marathon-Ready cDNA (Clontech Laboratories, Inc., Palo Alto, CA). The PCR was carried out using the Advantage™ cDNA PCR Kit (Clontech Laboratories, Inc., Palo Alto, CA) with 5 µl of human liver Marathon-Ready cDNA and 50 pmole each primer

following manufacturer's instructions. Thermocycler conditions in Perkin Elmer 9600 (Norwalk, CT) were as follows: 94 °C for 2 mins, then 30 cycles of 94 °C for 1 min., 58 °C for 2 mins., and 72 °C for 3 mins. PCR was followed by an additional extension at 72 °C for 7 mins.

Please replace the paragraph bridging pages 93 - 94 (i.e., page 93, line 11 - page 94, line 2) of the specification with the following paragraph:

The National Center for Biotechnology Information (NCBI at ~~http://www~~.ncbi.nlm.nin.gov) was used to conduct database searches using blastn with the mouse EST sequence AI225632 (see Example XIII). Three mouse EST sequences were identified (GenBank Accession #'s AI428130, AI595258, and AA061089), and assembled to generate a putative full-length elongation enzyme sequence, designated as MEL04. Primers RO819 (5' -ATG ATG CCA TGG AGC AGC TGA AGG CCT TTG- 3') (SEQ ID NO:83) and RO820 (5' -CAG TCT CTG CTT TAA AAC AAG GTC GTC- 3') (SEQ ID NO:84) were designed based on the putative full length mouse elongation enzyme sequence, and used to amplify the mouse brain Marathon-Ready cDNA (Clontech Laboratories, Inc., Palo Alto, California). The Polymerase Chain Reaction (PCR) was carried out as previously described (Example XVI). The PCR amplified product was run on a gel, an amplified fragment of approximately 1,000 bp was gel purified, the termini of the fragment were digested with NcoI and DraI (Boehringer Mannheim, Corp., Indianapolis, IN), and the fragment was cloned into pYX242 (NcoI/HindIII). The new plasmid was designated as pFAE-84, and the putative PUFA elongation enzyme cDNA in this clone was sequenced using ABI 373A Stretch DNA Sequencer (Perkin Elmer, Foster City, CA). The putative PUFA elongation enzyme cDNA sequence in plasmid pFAE-84 is shown in Figure 54, and the translated sequence is shown in Figure 55.

(Plasmid pRAE-84 was deposited with the American Type Culture Collection, 10802 University Boulevard, Manassas, VA 20110-2209, on July 25, 2000 and was accorded deposit number PTA-2262.)

Please replace the paragraph bridging pages 96-97 (i.e., page 96, line 11 - page 97, line 2) with the following paragraph:

The National Center for Biotechnology Information (NCBI at ~~http://www~~.ncbi.nlm.nih.gov) was used to conduct database searches using blastn with the HSELO1 sequence. Two human EST sequences were identified (GenBank Accession #'s AI787925 and AI746838) and the respective cDNA clones (I.M.A.G.E. Consortium Clone ID's 2076831 and 206182) were purchased through Research Genetics (Huntsville, AL). Primers RO833 (5' -GGT TTT ACC ATG GAA CAT TTC GAT GCG TCA C- 3') (SEQ ID NO:85) and RO832 (5' -CGA CCT GCA GCT CGA GCA CA- 3') (SEQ ID NO:86) were designed based on 5' sequence of the putative mouse elongation enzyme, and the cDNA clone vector, respectively. Primers RO833 and RO832 were used to amplify the mouse cDNA clone 2076182. The Polymerase Chain Reaction (PCR) was carried out as previously described (Example XVI). The termini of the PCR amplified product were filled-in with T4 DNA polymerase (Boehringer Mannheim, Corp., Indianapolis, IN) and the 5' region was digested with NcoI. The modified fragment was run on a gel, an amplified fragment of approximately 2.4 Kp was gel purified, and the fragment was cloned into pYX242 (NcoI/EcoRV). The new plasmid was designated as pRAE-87, and the putative PUFA elongation enzyme cDNA in this clone, MELO7, was sequenced using ABI 373A Stretch DNA Sequencer (Perkin Elmer, Foster City, CA). The putative PUFA elongation enzyme cDNA sequence in plasmid pRAE-87 (MELO7) is shown in Figure 58, and the translated sequence is shown in Figure 59. (The plasmid pRAE-87 was deposited with the American Type Culture Collection, 10802 University Boulevard, Manassas, VA 20110-2209, on July 25, 2000 and was accorded deposit number PTA-2261.)